Exhibit B

NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure
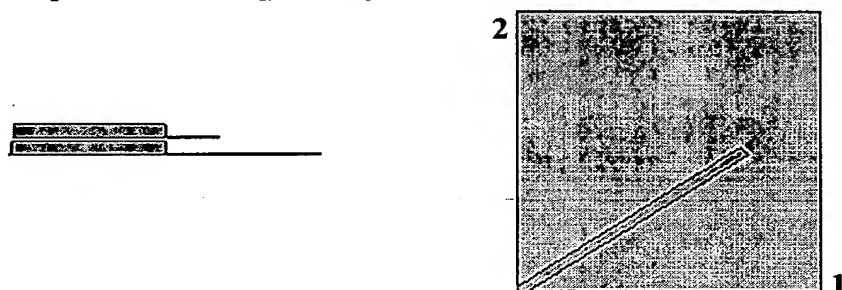
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.00000 wordsize: 11   Filter ☑   Align

Sequence 1 lcl|seq_1 **Length** 1414 (1 .. 1414)

Sequence 2 lcl|seq_2 **Length** 2112 (1 .. 2112)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 2021 bits (1051), Expect = 0.0
Identities = 1053/1054 (99%)
 Strand = Plus / Plus
```

SEQ ID NO: 1

BC 012074

```
Query: 1    aggacccgcgaggaagggcccgcggatggcgcgtccctgagggtcgtggcgagttcgcgg 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10   aggacccgcgaggaagggcccgcggatggcgcgtccctgagggtcgtggcgagttcgcgg 69


Query: 61   agcgtgggaaggagcggaccctgctctccccgggctgcgggccatggccacggcggagcg 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70   agcgtgggaaggagcggaccctgctctccccgggctgcgggccatggccacggcggagcg 129


Query: 121  gagagccctcggcatcggcttccagtggctctctttggccactctggtgctcatctgcgc 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 130  gagagccctcggcatcggcttccagtggctctctttggccactctggtgctcatctgcgc 189


Query: 181  cgggcaaggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 190  cgggcaaggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta 249
```

```
Query: 241   cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 250   cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 309


Query: 301   ggaacagttggctcacaaattcatcagcccacagttgagaatgtcctttattgttttctc 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 310   ggaacagttggctcacaaattcatcagcccacagttgagaatgtcctttattgttttctc 369


Query: 361   cacccgaggaacaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcct 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 370   cacccgaggaacaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcct 429


Query: 421   agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggatttgaaag 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 430   agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggatttgaaag 489


Query: 481   ggccagtgagcagatttattatgaaaacagacaagggtacaggacagccagcgtcatcat 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 490   ggccagtgagcagatttattatgaaaacagacaagggtacaggacagccagcgtcatcat 549


Query: 541   tgctttgactgatggagaactccatgaagatctcttttctattcagagagggaggctaa 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 550   tgctttgactgatggagaactccatgaagatctcttttctattcagagagggaggctaa 609


Query: 601   taggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagac 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 610   taggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagac 669


Query: 661   acagctggcccggattgcggacagtaaggatcatgtgtttcccgtgaatgacggctttca 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 670   acagctggcccggattgcggacagtaaggatcatgtgtttcccgtgaatgacggctttca 729


Query: 721   ggctctgcaaggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagc 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 730   ggctctgcaaggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagc 789


Query: 781   tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 790   tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt 849


Query: 841   ccgacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 850   ccgacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac 909


Query: 901   actcaatgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatctt 960
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 910   actcaatgagaagcccttttctgtggaagatacttatttactgtgtccagcgcctatctt 969
```

```
Query: 961   aaaagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttat 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 970   aaaagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttat 1029


Query: 1021  ctccagttctgtcatcatcaccaccacacactgt 1054
             ||||||||||||||||||||||||||||||||||
Sbjct: 1030  ctccagttctgtcatcatcaccaccacacactgt 1063
```

CPU time: 0.03 user secs.   0.00 sys. secs   0.03 total secs.

```
Lambda      K       H
    1.33    0.621    1.12

Gapped
Lambda      K       H
    1.33    0.621    1.12
```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 4
Number of Sequences: 0
Number of extensions: 4
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1414
length of database: 10,224,276,066
effective HSP length: 25
effective length of query: 1389
effective length of database: 10,224,276,041
effective search space: 14201519420949
effective search space used: 14201519420949
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)